

SEQUENCE LISTING

<110> Bayer Aktiengesellschaft

<120> Acetylcholine receptor subunits

<130> Le A 34 821

<140>

<141>

<150> DE 100 42 177.6

<151> 2000-08-28

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 45

<212> PRT

<213> Torpedo californica

<400> 1

Asp Phe Ala Ile Val His Met Thr Lys Leu Leu Leu Asp Tyr Thr Gly
1 5 10 15

Lys Ile Met Trp Thr Pro Pro Ala Ile Phe Lys Ser Tyr Cys Glu Ile
20 25 30

Ile Val Thr His Phe Pro Phe Asp Gln Gln Asn Cys Thr
35 40 45

<210> 2

<211> 1869

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1866)

<220>

<223> Description of Artificial Sequence: Modified alpha
4 subunit of the chicken nicotinic acetylcholine
receptor

<400> 2

atg gga ttt ctc gtg tcg aag gga aac ctc ctc ctc ctg ctg tgt gcc 48
Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala
1 5 10 15

agc atc ttc ccc gct ttc ggc cac gtg gaa acg cga gcc cat gcg gag Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu	20	25	30	96
gag cgc ctc ctg aag aaa ctc ttc tcc ggg tat aac aag tgg tcc cgt Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg	35	40	45	144
ccc gtc gcc aac att tcg gat gtg gtc ctg gtc cgc ttc ggc ttg tcc Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser	50	55	60	192
ata gcc cag ctc atc gat gtt gat gag aag aac caa atg atg acc aca Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr	65	70	75	240
aat gtg tgg gtg aag cag gag tgg cac gac tac aag ctg cgc tgg gac Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp	85	90	95	288
ccc cag gag tat gaa aac gtc aca tcc atc cga atc ccc tca gag ctc Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu	100	105	110	336
atc tgg cgg ccg gac ata gtc ctc tac aac aat gcc gac ggc aac ttc Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asn Phe	115	120	125	384
gag gta acg ctg gcg acg aag ggg act ttg aat tat acg gga cgt gtg Glu Val Thr Leu Ala Thr Lys Ala Thr Leu Asn Tyr Thr Gly Arg Val	130	135	140	432
gag tgg cgc ccg ccg gct atc tac aag tcc tgg tgg gag atc gac gtc Glu Trp Arg Pro Pro Ala Ile Tyr Lys Ser Ser Cys Glu Ile Asp Val	145	150	155	480
gaa tac ttc ccg ttc gac cag cag acg tgc gtc atg aag ttc ggc tgg Glu Tyr Phe Pro Phe Asp Gln Gln Thr Cys Val Met Lys Phe Gly Ser	165	170	175	528
tgg aca tat gac aaa gct aag ata gac ttg gtg agc atg cat agc cat Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His	180	185	190	576
gtg gac caa ctg gac tac tgg gaa acg ggg gag tgg gtc atc att aat Val Asp Gln Leu Asp Tyr Trp Glu Ser Gly Glu Trp Val Ile Ile Asn	195	200	205	624
gcc gtg ggc aat tac aac acg aag aaa tat gaa tgc tgc aca gag atc Ala Val Gly Asn Tyr Asn Ser Lys Lys Tyr Glu Cys Cys Thr Glu Ile	210	215	220	672
tac cct gat ata act tac tcc ttc att atc cgg agg ctg ccg ctg ttc Tyr Pro Asp Ile Thr Tyr Ser Phe Ile Ile Arg Arg Leu Pro Leu Phe				720

225	230	235	240	
tac aca atc aat ttg atc att ccc tgc ctg ctt atc tcc tgc ttg act				768
Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr				
245	250	255		
gtc ctg gtc ttc tac cta ccc tct gag tgc gga gag aag ata acc ttg				816
Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Ile Thr Leu				
260	265	270		
tgc atc tct gtg ctg cta tcc ctc acg gtg ttc ctg ctg ctc atc aca				864
Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Leu Ile Thr				
275	280	285		
gag atc atc cct tct acc tcc ctg gtc atc ccc ctg ata gga gag tat				912
Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr				
290	295	300		
ctg ctc ttc acc atg ata ttt gtc acc ttg tct atc atc atc act gtc				960
Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Ile Ile Thr Val				
305	310	315	320	
ttt gtg ctc aac gta cac cac cgt tca cca cgt acc cac acg atg cct				1008
Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Thr Met Pro				
325	330	335		
gac tgg gtg agg agg gtc ttc ctt gac ata gtc cca cgt ctc ctc ttc				1056
Asp Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe				
340	345	350		
atg aag cgg ccc tcc aca gtg aaa gac aat tgc aag aag ctt att gaa				1104
Met Lys Arg Pro Ser Thr Val Lys Asp Asn Cys Lys Leu Ile Glu				
355	360	365		
tct atg cac aaa cta acc aac tca cca agg ctt tgg tct gag acc gac				1152
Ser Met His Lys Leu Thr Asn Ser Pro Arg Leu Trp Ser Glu Thr Asp				
370	375	380		
atg gag ccc aac ttc act acc tca tcc tcc ccc agc ccc cag agt aat				1200
Met Glu Pro Asn Phe Thr Thr Ser Ser Ser Pro Ser Pro Gln Ser Asn				
385	390	395	400	
gaa cct tca ccc aca tct tcc ttc tgt gcc cac ctt gag gag cca gcc				1248
Glu Pro Ser Pro Thr Ser Ser Phe Cys Ala His Leu Glu Glu Pro Ala				
405	410	415		
aaa cct atg tgc aaa tcc cct tct gga cag tac tca atg ctg cac cct				1296
Lys Pro Met Cys Lys Ser Pro Ser Gly Gln Tyr Ser Met Leu His Pro				
420	425	430		
gag ccc cca cag gtg acg tgt tcc tct ccg aag ccc tcc tgc cac ccc				1344
Glu Pro Pro Gln Val Thr Cys Ser Ser Pro Lys Pro Ser Cys His Pro				
435	440	445		

ctg agt gac acc cag acc aca tct atc tca aaa ggc aga tcg ctc agt	1392
Leu Ser Asp Thr Gln Thr Ser Ile Ser Lys Gly Arg Ser Leu Ser	
450 455 460	
gtt cag cag atg tac agc ccc aat aag aca gag gaa ggg agc atc cgc	1440
Val Gln Gln Met Tyr Ser Pro Asn Lys Thr Glu Glu Gly Ser Ile Arg	
465 470 475 480	
tgt agg tcc cga agc atc cag tac tgt tac ctg cag gag gac tct tcc	1488
Cys Arg Ser Arg Ser Ile Gln Tyr Cys Tyr Leu Gln Glu Asp Ser Ser	
485 490 495	
cag acc aat ggc cac tct agt gcc tct cca gcg tcg cag cgc tgc cac	1536
Gln Thr Asn Gly His Ser Ser Ala Ser Pro Ala Ser Gln Arg Cys His	
500 505 510	
ctc aat gaa gag cag ccc cag cac aag ccc cac cag tgc aag tgt aag	1584
Leu Asn Glu Glu Gln Pro Gln His Lys Pro His Gln Cys Lys Cys Lys	
515 520 525	
tgc aga aag gga gag gca gct ggc aca ccg act caa gga agc aag agc	1632
Cys Arg Lys Gly Glu Ala Ala Gly Thr Pro Thr Gln Gly Ser Lys Ser	
530 535 540	
cac agc aac aaa gga gaa cac ctc gtg ctg atg tcc cca gcc ctg aag	1680
His Ser Asn Lys Gly Glu His Leu Val Leu Met Ser Pro Ala Leu Lys	
545 550 555 560	
ctg gcg gtg gaa ggg gtc cac tac att gca gac cac ctg cga gca gaa	1728
Leu Ala Val Glu Gly Val His Tyr Ile Ala Asp His Leu Arg Ala Glu	
565 570 575	
gat gca gat ttc tca gtg aag gaa gac tgg aag tac gta gca atg gtc	1776
Asp Ala Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val	
580 585 590	
att gac cgg atc ttt ctc tgg atg ttc atc gtg tgt ttg ctg ggg	1824
Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile Val Cys Leu Leu Gly	
595 600 605	
acc gtt ggg ctc ttc ctc ccg ccg tgg ctg gca gga atg atc taa	1869
Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala Gly Met Ile	
610 615 620	

<210> 3

<211> 622

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Modified alpha
4 subunit of the chicken nicotinic acetylcholine
receptor

<400> 3

Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala
1 5 10 15

Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu
20 25 30

Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg
35 40 45

Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser
50 55 60

Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr
65 70 75 80

Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp
85 90 95

Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu
100 105 110

Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asn Phe
115 120 125

Glu Val Thr Leu Ala Thr Lys Ala Thr Leu Asn Tyr Thr Gly Arg Val
130 135 140

Glu Trp Arg Pro Pro Ala Ile Tyr Lys Ser Ser Cys Glu Ile Asp Val
145 150 155 160

Glu Tyr Phe Pro Phe Asp Gln Gln Thr Cys Val Met Lys Phe Gly Ser
165 170 175

Trp Thr Tyr Asp Ala Lys Ile Asp Leu Val Ser Met His Ser His
180 185 190

Val Asp Gln Leu Asp Tyr Trp Glu Ser Gly Glu Trp Val Ile Ile Asn
195 200 205

Ala Val Gly Asn Tyr Asn Ser Lys Lys Tyr Glu Cys Cys Thr Glu Ile
210 215 220

Tyr Pro Asp Ile Thr Tyr Ser Phe Ile Ile Arg Arg Leu Pro Leu Phe
225 230 235 240

Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr
245 250 255

Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Ile Thr Leu
260 265 270

Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Ile Thr
275 280 285

TOZ200-6770001

Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr
 290 295 300
 Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Ile Ile Thr Val
 305 310 315 320
 Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Thr Met Pro
 325 330 335
 Asp Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe
 340 345 350 355
 Met Lys Arg Pro Ser Thr Val Lys Asp Asn Cys Lys Lys Leu Ile Glu
 355 360 365
 Ser Met His Lys Leu Thr Asn Ser Pro Arg Leu Trp Ser Glu Thr Asp
 370 375 380
 Met Glu Pro Asn Phe Thr Thr Ser Ser Ser Pro Ser Pro Gln Ser Asn
 385 390 395 400
 Glu Pro Ser Pro Thr Ser Ser Phe Cys Ala His Leu Glu Glu Pro Ala
 405 410 415
 Lys Pro Met Cys Lys Ser Pro Ser Gly Gln Tyr Ser Met Leu His Pro
 420 425 430
 Glu Pro Pro Gln Val Thr Cys Ser Ser Pro Lys Pro Ser Cys His Pro
 435 440 445
 Leu Ser Asp Thr Gln Thr Thr Ser Ile Ser Lys Gly Arg Ser Leu Ser
 450 455 460
 Val Gln Gln Met Tyr Ser Pro Asn Lys Thr Glu Glu Gly Ser Ile Arg
 465 470 475 480
 Cys Arg Ser Arg Ser Ile Gln Tyr Cys Tyr Leu Gln Glu Asp Ser Ser
 485 490 495
 Gln Thr Asn Gly His Ser Ser Ala Ser Pro Ala Ser Gln Arg Cys His
 500 505 510
 Leu Asn Glu Glu Gln Pro Gln His Lys Pro His Gln Cys Lys Cys Lys
 515 520 525
 Cys Arg Lys Gly Glu Ala Ala Gly Thr Pro Thr Gln Gly Ser Lys Ser
 530 535 540
 His Ser Asn Lys Gly Glu His Leu Val Leu Met Ser Pro Ala Leu Lys
 545 550 555 560
 Leu Ala Val Glu Gly Val His Tyr Ile Ala Asp His Leu Arg Ala Glu
 565 570 575

Asp Ala Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val
580 585 590
Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile Val Cys Leu Leu Gly
595 600 605
Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala Gly Met Ile
610 615 620

<210> 4
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 4
cacgtgcctt ccgagctcat ctggcgccg g

31

<210> 5
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 5
gtcatatgtc cacgagccga ac

22

<210> 6
<211> 1896
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1893)

<220>
<223> Description of Artificial Sequence: Modified alpha
4 subunit of the chicken nicotinic acetylcholine
receptor

<400> 6
atg gga ttt ctc gtg tcg aag gga aac ctc ctc ctc ctg ctg tgc ggc
Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala
1 5 10 15

agc atc ttc ccc gct ttc ggc cac gtg gaa acg cga gcc cat gcg gag Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu 20 25 30	96
gag cgc ctc ctg aag aaa ctc ttc tcc ggg tat aac aag tgg tcc cgt Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg 35 40 45	144
ccc gtc gcc aac att tcg gat gtg gtc ctg gtc cgc ttc ggc ttg tcc Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser 50 55 60	192
ata gcc cag ctc atc gat gtt gat gag aag aac caa atg atg acc aca Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr 65 70 75 80	240
aat gtg tgg gtg aag cag gag tgg cac gac tac aag ctg cgc tgg gac Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp 85 90 95	288
ccc cag gag tat gaa aac gtc aca tcc atc cga atc ccc tca gag ctc Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu 100 105 110	336
atc tgg agg ccg gac att gtc cta tac aac aat gct gat ggt gac ttt Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe 115 120 125	384
gca gtc acc cac ctg acc aaa gcc cac ctc ttc tat gat ggg aga att Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile 130 135 140	432
aaa tgg atg cca cct gcc atc tac aaa agc tcc tgc agc atc gat gtt Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val 145 150 155 160	480
acc ttc ttc ccc ttt gat cag caa aac tgt aaa atg aaa ttt ggc tct Thr Phe Pro Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser 165 170 175	528
tgg aca tat gac aaa gct aag ata gac ttg gtg agc atg cat agc cat Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His 180 185 190	576
cgc ggg acc aac gtg gtg gag ctg ggc gtg gac caa ctg gac tac tgg Arg Gly Thr Asn Val Val Glu Leu Gly Val Asp Gln Leu Asp Tyr Trp 195 200 205	624
gaa agc ggg gag tgg gtc atc att aat gcc gtg ggc aat tac aac agc Glu Ser Gly Glu Trp Val Ile Ile Asn Ala Val Gly Asn Tyr Asn Ser 210 215 220	672
aag aaa tat gaa tgc tgc aca gag atc tac cct gat ata act tac tcc Lys Lys Tyr Glu Cys Cys Thr Glu Ile Tyr Pro Asp Ile Thr Tyr Ser	720

225	230	235	240	
ttc att atc cgg agg ctg ccg ctg ttc tac aca atc aat ttg atc att Phe Ile Ile Arg Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile 245 250 255				768
ccc tgc ctg ctt atc tcc tgc ttg act gtc ctg gtc ttc tac cta ccc Pro Cys Leu Leu Ile Ser Cys Leu Thr Val Leu Val Phe Tyr Leu Pro 260 265 270				816
tct gag tgc gga gag aag ata acc ttg tgc atc tct gtg ctg cta tcc Ser Glu Cys Gly Glu Lys Ile Thr Leu Cys Ile Ser Val Leu Leu Ser 275 280 285				864
ctc acg gtg ttc ctg ctg ctc atc aca gag atc atc cct tct acc tcc Leu Thr Val Phe Leu Leu Ile Thr Glu Ile Ile Pro Ser Thr Ser 290 295 300				912
ctg gtc atc ccc ctg ata gga gag tat ctg ctc ttc acc atg ata ttt Leu Val Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe 305 310 315 320				960
gtc acc ttg tct atc atc act gtc ttt gtg ctc aac gta cac cac Val Thr Leu Ser Ile Ile Ile Thr Val Phe Val Leu Asn Val His His 325 330 335				1008
cgt tca cca cgt acc cac acg atg cct gac tgg gtg agg agg gtc ttc Arg Ser Pro Arg Thr His Thr Met Pro Asp Trp Val Arg Arg Val Phe 340 345 350				1056
ctt gac ata gtc cca cgt ctc ctc ttc atg aag cgg ccc tcc aca gtg Leu Asp Ile Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser Thr Val 355 360 365				1104
aaa gac aat tgc aag aag ctt att gaa tct atg cac aaa cta acc aac Lys Asp Asn Cys Lys Lys Leu Ile Glu Ser Met His Lys Leu Thr Asn 370 375 380				1152
tca cca agg ctt tgg tct gag acc gac atg gag ccc aac ttc act acc Ser Pro Arg Leu Trp Ser Glu Thr Asp Met Glu Pro Asn Phe Thr Thr 385 390 395 400				1200
tca tcc tcc ccc agc ccc cag agt aat gaa cct tca ccc aca tct tcc Ser Ser Ser Pro Ser Pro Gln Ser Asn Glu Pro Ser Pro Thr Ser Ser 405 410 415				1248
ttc tgt gcc cac ctt gag gag cca gcc aaa cct atg tgc aaa tcc cct Phe Cys Ala His Leu Glu Glu Pro Ala Lys Pro Met Cys Lys Ser Pro 420 425 430				1296
tct gga cag tac tca atg ctg cac cct gag ccc cca cag gtg acg tgt Ser Gly Gln Tyr Ser Met Leu His Pro Glu Pro Pro Gln Val Thr Cys 435 440 445				1344

tcc tct ccg aag ccc tcc tgc cac ccc ctg agt gac acc cag acc aca Ser Ser Pro Lys Pro Ser Cys His Pro Leu Ser Asp Thr Gln Thr Thr 450 455 460	1392
tct atc tca aaa ggc aga tcg ctc agt gtt cag cag atg tac agc ccc Ser Ile Ser Lys Gly Arg Ser Leu Ser Val Gln Gln Met Tyr Ser Pro 465 470 475 480	1440
aat aag aca gag gaa ggg agc atc cgc tgt agg tcc cga agc atc cag Asn Lys Thr Glu Glu Gly Ser Ile Arg Cys Arg Ser Arg Ser Ile Gln 485 490 495	1488
tac tgt tac ctg cag gag gac tct tcc cag acc aat ggc cac tct agt Tyr Cys Tyr Leu Gln Glu Asp Ser Ser Gln Thr Asn Gly His Ser Ser 500 505 510	1536
gcc tct cca gcg tcg cag cgc tgc cac ctc aat gaa gag cag ccc cag Ala Ser Pro Ala Ser Gln Arg Cys His Leu Asn Glu Glu Gln Pro Gln 515 520 525	1584
cac aag ccc cac cag tgc aag tgt aag tgc aga aag gga gag gca gct His Lys Pro His Gln Cys Lys Cys Lys Cys Arg Lys Gly Glu Ala Ala 530 535 540	1632
ggc aca ccg act caa gga agc aag agc cac agc aac aaa gga gaa cac Gly Thr Pro Thr Gln Gly Ser Lys Ser His Ser Asn Lys Gly Glu His 545 550 555 560	1680
ctc gtg ctg atg tcc cca gcc ctg aag ctg gcg gtg gaa ggg gtc cac Leu Val Leu Met Ser Pro Ala Leu Lys Leu Ala Val Glu Gly Val His 565 570 575	1728
tac att gca gac cac ctg cga gca gaa gat gca gat ttc tca gtg aag Tyr Ile Ala Asp His Leu Arg Ala Glu Asp Ala Asp Phe Ser Val Lys 580 585 590	1776
gaa gac tgg aag tac gta gca atg gtc att gac cgg atc ttt ctc tgg Glu Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp 595 600 605	1824
atg ttc atc atc gtg tgt ttg ctg ggg acc gtt ggg ctc ttc ctc ccg Met Phe Ile Ile Val Cys Leu Leu Gly Thr Val Gly Leu Phe Leu Pro 610 615 620	1872
ccg tgg ctg gca gga atg atc taa Pro Trp Leu Ala Gly Met Ile 625 630	1896

<210> 7

<211> 631

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Modified alpha

4 subunit of the chicken nicotinic acetylcholine
receptor

<400> 7
Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala
1 5 10 15
Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu
20 25 30
Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg
35 40 45
Pro Val Ala Asn Ile Ser Asp Val Val Leu Arg Phe Gly Leu Ser
50 55 60
Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr
65 70 75 80
Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp
85 90 95
Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu
100 105 110
Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe
115 120 125
Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile
130 135 140
Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val
145 150 155 160
Thr Phe Pro Phe Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser
165 170 175
Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His
180 185 190
Arg Gly Thr Asn Val Val Glu Leu Gly Val Asp Gln Leu Asp Tyr Trp
195 200 205
Glu Ser Gly Glu Trp Val Ile Ile Asn Ala Val Gly Asn Tyr Asn Ser
210 215 220
Lys Lys Tyr Glu Cys Cys Thr Glu Ile Tyr Pro Asp Ile Thr Tyr Ser
225 230 235 240
Phe Ile Ile Arg Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile
245 250 255
Pro Cys Leu Leu Ile Ser Cys Leu Thr Val Leu Val Phe Tyr Leu Pro
260 265 270

Ser Glu Cys Gly Glu Lys Ile Thr Leu Cys Ile Ser Val Leu Leu Ser
 275 280 285
 Leu Thr Val Phe Leu Leu Leu Ile Thr Glu Ile Ile Pro Ser Thr Ser
 290 295 300
 Leu Val Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe
 305 310 315 320
 Val Thr Leu Ser Ile Ile Ile Thr Val Phe Val Leu Asn Val His His
 325 330 335
 Arg Ser Pro Arg Thr His Thr Met Pro Asp Trp Val Arg Arg Val Phe
 340 345 350
 Leu Asp Ile Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser Thr Val
 355 360 365
 Lys Asp Asn Cys Lys Lys Leu Ile Glu Ser Met His Lys Leu Thr Asn
 370 375 380
 Ser Pro Arg Leu Trp Ser Glu Thr Asp Met Glu Pro Asn Phe Thr Thr
 385 390 395 400
 Ser Ser Ser Pro Ser Pro Gln Ser Asn Glu Pro Ser Pro Thr Ser Ser
 405 410 415
 Phe Cys Ala His Leu Glu Glu Pro Ala Lys Pro Met Cys Lys Ser Pro
 420 425 430
 Ser Gly Gln Tyr Ser Met Leu His Pro Glu Pro Pro Gln Val Thr Cys
 435 440 445
 Ser Ser Pro Lys Pro Ser Cys His Pro Leu Ser Asp Thr Gln Thr Thr
 450 455 460
 Ser Ile Ser Lys Gly Arg Ser Leu Ser Val Gln Gln Met Tyr Ser Pro
 465 470 475 480
 Asn Lys Thr Glu Glu Gly Ser Ile Arg Cys Arg Ser Arg Ser Ile Gln
 485 490 495
 Tyr Cys Tyr Leu Gln Glu Asp Ser Ser Gln Thr Asn Gly His Ser Ser
 500 505 510
 Ala Ser Pro Ala Ser Gln Arg Cys His Leu Asn Glu Glu Gln Pro Gln
 515 520 525
 His Lys Pro His Gln Cys Lys Cys Lys Cys Arg Lys Gly Glu Ala Ala
 530 535 540
 Gly Thr Pro Thr Gln Gly Ser Lys Ser His Ser Asn Lys Gly Glu His
 545 550 555 560

Leu Val Leu Met Ser Pro Ala Leu Lys Leu Ala Val Glu Gly Val His
565 570 575
Tyr Ile Ala Asp His Leu Arg Ala Glu Asp Ala Asp Phe Ser Val Lys
580 585 590
Glu Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp
595 600 605
Met Phe Ile Ile Val Cys Leu Leu Gly Thr Val Gly Leu Phe Leu Pro
610 615 620
Pro Trp Leu Ala Gly Met Ile
625 630

PRIMER: 5'-CTTGGGCG

<210> 8
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
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gtggaccaac tggactactg g 81

<210> 9
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
ccagtagtcc agttggtcca cacccagttc taccacgttg gttcctctag cctcatcgat 60
gtgtctcaag tctatcttag c 81

<210> 10
<211> 1869
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1866)

<220>

<223> Description of Artificial Sequence: Modified alpha 4 subunit of the chicken nicotinic acetylcholine receptor

atg gga ttt ctc gtg tcg aag gga aac ctc ctc ctc ctg ctg tgt gcc	48
Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala	
1 5 10 15	
agc atc ttc ccc gct ttc ggc cac gtg gaa acg cga gcc cat gcg gag	96
Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu	
20 25 30	
gag cgc ctc ctg aag aaa ctc ttc tcc ggg tat aac aag tgg tcc cgt	144
Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg	
35 40 45	
ccc gtc gcc aac att tcg gat gtg gtc ctg gtc cgc ttc ggc ttg tcc	192
Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser	
50 55 60	
ata gcc cag ctc atc gat gtt gat gag aag aac caa atg atg acc aca	240
Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr	
65 70 75 80	
aat gtg tgg gtg aag cag gag tgg cac gac tac aag ctg cgc tgg gac	288
Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp	
85 90 95	
ccc cag gag tat gaa aac gtc aca tcc atc cga atc ccc tca gag ctc	336
Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu	
100 105 110	
atc tgg agg ccg gac att gtc cta tac aac aat gct gat ggt gac ttt	384
Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe	
115 120 125	
gca gtc acc cac ctg acc aaa gcc cac ctc ttc tat gat ggg aga att	432
Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile	
130 135 140	
aaa tgg atg cca cct gcc atc tac aaa agc tcc tgc agc atc gat gtt	480
Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val	
145 150 155 160	
acc ttc ttc ccc ttt gat cag caa aac tgt aaa atg aaa ttt ggc tct	528
Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser	
165 170 175	
tgg aca tat gac aaa gct aag ata gac ttc gtg agc atg cat agc cat	576
Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His	
180 185 190	
gtc gac ctg tcc gag ttc tac acc tcc gtg gag tgg gac atc ctg gag	624

Val	Asp	Leu	Ser	Glu	Phe	Tyr	Thr	Ser	Val	Glu	Trp	Asp	Ile	Leu	Glu	
		195			200						205					
gtg	cca	gcc	gtc	agg	aac	gag	aag	ttc	tac	acg	tgc	tgc	gac	gag	ccc	672
Val	Pro	Ala	Val	Arg	Asn	Glu	Lys	Phe	Tyr	Thr	Cys	Cys	Asp	Glu	Pro	
210					215						220					
tac	ctg	gac	ata	acg	ttt	aac	ttc	att	atc	cg	agg	ctg	ccg	ctg	ttc	720
Tyr	Leu	Asp	Ile	Thr	Phe	Asn	Phe	Ile	Ile	Arg	Arg	Leu	Pro	Leu	Phe	
225					230					235			240			
tac	aca	atc	aat	ttg	atc	att	ccc	tgc	ctg	ctt	atc	tcc	tgc	ttg	act	768
Tyr	Thr	Ile	Asn	Leu	Ile	Ile	Pro	Cys	Leu	Leu	Ile	Ser	Cys	Leu	Thr	
					245				250			255				
gtc	ctg	gtc	ttc	tac	cta	ccc	tct	gag	tgc	gga	gag	aag	ata	acc	ttg	816
Val	Leu	Val	Phe	Tyr	Leu	Pro	Ser	Glu	Cys	Gly	Glu	Lys	Ile	Thr	Leu	
					260			265			270					
tgc	atc	tct	gtg	ctg	cta	tcc	ctc	acg	gtg	ttc	ctg	ctg	ctc	atc	aca	864
Cys	Ile	Ser	Val	Leu	Leu	Ser	Leu	Thr	Val	Phe	Leu	Leu	Leu	Ile	Thr	
					275			280			285					
gag	atc	atc	cct	tct	acc	tcc	ctg	gtc	atc	ccc	ctg	ata	gga	gag	tat	912
Glu	Ile	Ile	Pro	Ser	Thr	Ser	Leu	Val	Ile	Pro	Leu	Ile	Gly	Glu	Tyr	
					290			295			300					
ctg	ctc	tcc	acc	atg	ata	ttt	gtc	acc	ttg	tct	atc	atc	atc	act	gtc	960
Leu	Leu	Phe	Thr	Met	Ile	Phe	Val	Thr	Leu	Ser	Ile	Ile	Ile	Ile	Thr	
					305			310			315			320		
ttt	gtg	ctc	aac	gta	cac	cac	cgt	tca	cca	cgt	acc	cac	acg	atg	cct	1008
Phe	Val	Leu	Asn	Val	His	His	Arg	Ser	Pro	Arg	Thr	His	Thr	Met	Pro	
					325			330			335					
gac	tgg	gtg	agg	agg	gtc	ttc	ctt	gac	ata	gtc	cca	cgt	ctc	ctc	ttc	1056
Asp	Trp	Val	Arg	Arg	Val	Phe	Leu	Asp	Ile	Val	Pro	Arg	Leu	Leu	Phe	
					340			345			350					
atg	aag	cgg	ccc	tcc	aca	gtg	aaa	gac	aat	tgc	aag	ttt	att	gaa		1104
Met	Lys	Arg	Pro	Ser	Thr	Val	Lys	Asp	Asn	Cys	Lys	Lys	Leu	Ile	Glu	
					355			360			365					
tct	atg	cac	aaa	cta	acc	aac	tca	cca	agg	ctt	tgg	tct	gag	acc	gac	1152
Ser	Met	His	Lys	Leu	Thr	Asn	Ser	Pro	Arg	Leu	Trp	Ser	Glu	Thr	Asp	
					370			375			380					
atg	gag	ccc	aac	ttc	act	acc	tca	tcc	tcc	ccc	agc	ccc	cag	agt	aat	1200
Met	Glu	Pro	Asn	Phe	Thr	Thr	Ser	Ser	Ser	Pro	Ser	Pro	Gln	Ser	Asn	
					385			390			395			400		
gaa	cct	tca	ccc	aca	tct	tcc	ttc	tgt	gcc	cac	ctt	gag	gag	cca	gcc	1248
Glu	Pro	Ser	Pro	Thr	Ser	Ser	Phe	Cys	Ala	His	Leu	Glu	Glu	Pro	Ala	
					405			410			415					

aaa cct atg tgc aaa tcc cct tct gga cag tac tca atg ctg cac cct	1296
Lys Pro Met Cys Lys Ser Pro Ser Gly Gln Tyr Ser Met Leu His Pro	
420 425 430	
gag ccc cca cag gtg acg tgt tcc tct ccg aag ccc tcc tgc cac ccc	1344
Glu Pro Pro Gln Val Thr Cys Ser Ser Pro Lys Pro Ser Cys His Pro	
435 440 445	
ctg agt gac acc cag acc aca tct atc tca aaa ggc aga tcg ctc agt	1392
Leu Ser Asp Thr Gln Thr Ser Ile Ser Lys Gly Arg Ser Leu Ser	
450 455 460	
gtt cag cag atg tac agc ccc aat aag aca gag gaa ggg agc atc cgc	1440
Val Gln Gln Met Tyr Ser Pro Asn Lys Thr Glu Glu Gly Ser Ile Arg	
465 470 475 480	
tgt agg tcc cga agc atc cag tac tgt tac ctg cag gag gac tct tcc	1488
Cys Arg Ser Arg Ser Ile Gln Tyr Cys Tyr Leu Gln Glu Asp Ser Ser	
485 490 495	
cag acc aat ggc cac tct agt gcc tct cca gcg tcg cag cgc tgc cac	1536
Gln Thr Asn Gly His Ser Ser Ala Ser Pro Ala Ser Gln Arg Cys His	
500 505 510	
ctc aat gaa gag cag ccc cac aag ccc cac cag tgc aag tgt aag	1584
Leu Asn Glu Gln Pro Gln His Lys Pro His Gln Cys Lys Cys Lys	
515 520 525	
tgc aga aag gga gag gca gct ggc aca ccg act caa gga agc aag agc	1632
Cys Arg Lys Gly Glu Ala Ala Gly Thr Pro Thr Gln Gly Ser Lys Ser	
530 535 540	
cac agc aac aaa gga gaa cac ctc gtg ctg atg tcc cca gcc ctg aag	1680
His Ser Asn Lys Gly Glu His Leu Val Leu Met Ser Pro Ala Leu Lys	
545 550 555 560	
ctg gcg gtg gaa ggg gtc cac tac att gca gac cac ctg cga gca gaa	1728
Leu Ala Val Glu Gly Val His Tyr Ile Ala Asp His Leu Arg Ala Glu	
565 570 575	
gat gca gat ttc tca gtg aag gaa gac tgg aag tac gta gca atg gtc	1776
Asp Ala Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val	
580 585 590	
att gac cgg atc ttt ctc tgg atg ttc atc atc gtg tgt ttg ctg ggg	1824
Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile Val Cys Leu Leu Gly	
595 600 605	
acc gtt ggg ctc ttc ctc ccg ccg tgg ctg gca gga atg atc taa	1869
Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala Gly Met Ile	
610 615 620	

<210> 11
<211> 622
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Modified alpha
4 subunit of the chicken nicotinic acetylcholine
receptor

<400> 11
Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala
1 5 10 15
Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu
20 25 30
Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg
35 40 45
Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser
50 55 60
Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr
65 70 75 80
Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp
85 90 95
Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu
100 105 110
Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe
115 120 125
Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile
130 135 140
Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val
145 150 155 160
Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser
165 170 175
Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His
180 185 190
Val Asp Leu Ser Glu Phe Tyr Thr Ser Val Glu Trp Asp Ile Leu Glu
195 200 205
Val Pro Ala Val Arg Asn Glu Lys Phe Tyr Thr Cys Cys Asp Glu Pro
210 215 220
Tyr Leu Asp Ile Thr Phe Asn Phe Ile Ile Arg Arg Leu Pro Leu Phe
225 230 235 240

Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr
 245 250 255
 Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Ile Thr Leu
 260 265 270
 Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Leu Ile Thr
 275 280 285
 Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr
 290 295 300
 Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Ile Ile Thr Val
 305 310 315 320
 Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Thr Met Pro
 325 330 335
 Asp Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe
 340 345 350
 Met Lys Arg Pro Ser Thr Val Lys Asp Asn Cys Lys Lys Leu Ile Glu
 355 360 365
 Ser Met His Lys Leu Thr Asn Ser Pro Arg Leu Trp Ser Glu Thr Asp
 370 375 380
 Met Glu Pro Asn Phe Thr Thr Ser Ser Ser Pro Ser Pro Gln Ser Asn
 385 390 395 400
 Glu Pro Ser Pro Thr Ser Ser Phe Cys Ala His Leu Glu Glu Pro Ala
 405 410 415
 Lys Pro Met Cys Lys Ser Pro Ser Gly Gln Tyr Ser Met Leu His Pro
 420 425 430
 Glu Pro Pro Gln Val Thr Cys Ser Ser Pro Lys Pro Ser Cys His Pro
 435 440 445
 Leu Ser Asp Thr Gln Thr Thr Ser Ile Ser Lys Gly Arg Ser Leu Ser
 450 455 460
 Val Gln Gln Met Tyr Ser Pro Asn Lys Thr Glu Glu Gly Ser Ile Arg
 465 470 475 480
 Cys Arg Ser Arg Ser Ile Gln Tyr Cys Tyr Leu Gln Glu Asp Ser Ser
 485 490 495
 Gln Thr Asn Gly His Ser Ser Ala Ser Pro Ala Ser Gln Arg Cys His
 500 505 510
 Leu Asn Glu Glu Gln Pro Gln His Lys Pro His Gln Cys Lys Cys Lys
 515 520 525

Cys Arg Lys Gly Glu Ala Ala Gly Thr Pro Thr Gln Gly Ser Lys Ser
530 535 540

His Ser Asn Lys Gly Glu His Leu Val Leu Met Ser Pro Ala Leu Lys
545 550 555 560

Leu Ala Val Glu Gly Val His Tyr Ile Ala Asp His Leu Arg Ala Glu
565 570 575

Asp Ala Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val
580 585 590

Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile Val Cys Leu Leu Gly
595 600 605

Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala Gly Met Ile
610 615 620

<210> 12
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
caacagcaag aaatatgaat gctgcgacga gccctacctt gatataactt tcaacttcat 60
tatccggagg ctgcccgtg 79

<210> 13
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 13
cagcggcagc ctccggataa tgaagttgaa agttatatca aggttagggct cgtgcagca 60
ttcatatttc ttgctgttg 79

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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<400> 14
gaacaaaagc tggaggtcca ccgcgggtggc 30

<210> 15
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
gccaccgcgg tggacacctca gcttttggc 30

<210> 16
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
gcggggagtg ggtcatctta gaagtcccg ccgttcgcaa cgaaaagttt tatacatgct 60
gacgacgagcc ctacc 75

<210> 17
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
ggtagggctc gtcgcagcat gtataaaact tttcggtcg aacggccggg acttcaatga 60
tgacccactc cccgc